between departments was required to facilitate the investigation, screening, and PEP process.

Results: 294 HCWs were identified as having physical contact with the organ recipients. 272 HCWs were considered low risk not requiring PEP. 12 were lost to follow-up due to resignation. 10 HCWs received PEP: 3 due to a high risk procedure, 2 with an unreported splash exposure, and 5 due to an unsure exposure risk. 5 HCWs indicated inappropriate personal protective equipment use. No HCW developed RVD.

Conclusion: The investigation identified areas for improvement; poor compliance with infection control practices, underreporting of exposures, and organ donations from high risk countries to include screening for RVD if cause of death is associated with non-specific encephalitis.

http://dx.doi.org/10.1016/j.ijid.2016.02.480

Type: Poster Presentation

Final Abstract Number: 42.010
Session: Poster Session II
Date: Friday, March 4, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Real time antimicrobial resistance surveillance in critical care: Identifying outbreaks of carbapenem resistant gram negative bacteria from routinely collected data

L.S.P. Moore[1], R. Freeman[2], A. Charlett[2], J.A. otter[3], H. Donaldson[3], A.H. Holmes[1,*]

[1] *Imperial College London, London, United Kingdom*
[2] *Public Health England, London, United Kingdom*
[3] *Imperial College Healthcare NHS Trust, London, United Kingdom*

Background: Statistically significant variation in antimicrobial resistance (AMR) occurs between hospitals, within hospitals, and over time. Whilst case mix and antimicrobial use contribute, the impact of cross-transmission on these fluctuations is not well understood. We investigated the utility of applying a statistical algorithm to identify outbreaks of carbapenem-resistant infections across three critical care units in a multi-centre teaching hospital network serving a population of 2 million in London, UK.

Methods & Materials: We applied a negative binomial regression model which accounts for seasonality and linear trends, as described by Noufaily *et al.*, to routinely collected microbiology data (fiscal years 2009-2015 for two units, 2012-2015 for the third) for carbapenem-resistant *Pseudomonas* spp. and Enterobacteriaceae (CRE). The first two years of data for each unit was used to train the algorithm. Exceedances (i.e. weeks with possible outbreaks) were validated by antibiogram comparison (as a proxy-indicator of strain similarity), against hospital infection control reports, and where available through genotypic typing.

Results: Across the three units, 154 CRE (from 3640 Enterobacteriaceae) were identified. The algorithm identified 17 exceedance weeks, in 11 multi-week clusters. In four of these clusters (three *K. pneumoniae*, one *E. coli*) organisms shared identical antibiograms; typing was available for one *K. pneumoniae* cluster, indicating clonal NDM cross-transmission, and this was the only outbreak (of the 11 clusters) identified in hospital infection control reports. Among 786 carbapenem-resistant *Pseudomonas* spp. (from 2378 isolated), 27 exceedance weeks were detected, in 15 multi-week clusters. Organisms in eight clusters shared identical antibiograms. No typing was available and none of the clusters had been identified in hospital infection control reports. No additional outbreaks of CRE or carbapenem-resistant *Pseudomonas* spp. were identified through routine surveillance or in hospital infection control reports.

Conclusion: The rise of carbapenem resistant organisms necessitates low-cost, easy-to-use surveillance mechanisms to aid early identification of outbreaks, particularly in critical care. Our data suggests such outbreaks may be more common than previously thought, and may be going undetected by current surveillance systems. Application of the Noufaily algorithm to routinely collected microbiology data provides a valid mechanism to better target limited hospital epidemiology, infection control, and diagnostics resources.

http://dx.doi.org/10.1016/j.ijid.2016.02.481

Type: Poster Presentation

Final Abstract Number: 42.011
Session: Poster Session II
Date: Friday, March 4, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Relationships between flavivirus serological laboratory test results from dengue endemic areas of India: Limitations and challenges

J. Nealon[1,*], A. Chakravarti[2], A. Moureau[3], S. Kumar[2], L. Ochiai[4], M. Bonaparte[5], S. Garg[2]

[1] *Sanofi Pasteur, Singapore, Singapore*
[2] *Maulana Azad Medical College, New Delhi, India*
[3] *Sanofi Pasteur, Marcy l'Etoile, France*
[4] *Sanofi Pasteur, Lyons, United Kingdom*
[5] *Sanofi Pasteur, Swiftwater, USA*

Background: Cross-sectional, population-based seroprevalence studies provide data on exposure to pathogens, susceptibility and disease transmission dynamics, and are useful in public health and vaccination planning. Cross-reactivity between flavivirus IgG antibody assays is an important consideration where multiple flaviviruses co-circulate.

Methods & Materials: An age-stratified dengue and Japanese encephalitis virus (JEV) IgG seroprevalence study was conducted in 8 sites across India, enrolling 2,591 subjects aged 5 – 10 years. Sera were tested using commercial ELISA kits; those dengue positive were subjected to plaque reduction neutralization test (PRNT) for serotype-specific neutralizing antibodies (DEN-1, 2, 3 and 4). A threshold of $\geq$ 10 (1/dil) was considered detectable; an algorithm was applied to interpret profiles as "naïve", "monotypic" or "multitypic". This secondary analysis explored a hypothesis that JEV IgG status was associated with cross-reactive dengue antibodies. JEV IgG results were analyzed by: a) dengue IgG status; b) naïve/monotypic/multitypic PRNT profile; c) the number of serotypes with detectable neutralizing antibodies; and d) geometric mean neutralizing antibody titer (GMT). Associations were tested by Pearson's chi squared test.

Results: Overall, 1,525/2,558 (59.6%) of available samples were dengue IgG positive, and 345/2,544 (13.6%) were positive for JEV IgG. Of JEV positive samples, 327 (94.8%) were also dengue IgG positive. Similarly, 96.5% of the 405 "inconclusive" JEV samples were dengue positive. Of the 1,794 JEV IgG negative samples, 801 (44.6%) were dengue IgG positive ($p<0.0001$). Examining PRNT profiles, 0.62%, 25.3% and 74.1% of JEV positive samples were naïve, monotypic and multitypic, compared to 4.5%, 38.6% and 56.9% of JEV